| Designation | Species | Epitope | Western Blot | E<br>E | FACS | Epitope sequence       |
|-------------|---------|---------|--------------|--------|------|------------------------|
|             |         |         |              |        |      |                        |
| 29C11       | rabbit  | Pro2    | Yes          | yes**  | n.d. | IDELKECFLNQTDETLSNVE   |
| 31A5        | rabbit  | Pro3    | Yes          | yes**  | yes  | ELLOEFIDDNATTNAIDELK   |
| 6A1         | rabbit  | Pro2-3  | Yes          | n.d.   | . 01 | TTNAIDELKECFLNO        |
| 14A12       | rabbit  | Pro3    | Yes          | n.d.   | yes  | ELLOEFIDDNATTNAIDELK   |
| 6812        | rabbit  | Pro3    | Yes          | n.d.   | yes  | ELLOEFIDDNATTNAIDELK   |
| 203         | rabbit  | Pro5    | Yes          | n.d.   | yes  | SOHCYAGSGCPLLENVISKTI  |
| 1608        | rabbit  | Pro3    | Yes          | n.d.   | yes  | ELLOEFIDDNATTNAIDELK   |
| 31-1H7      | mouse   | n.d.    | Yes          | n.d.   | yes  |                        |
| 197-1H11    | mouse   | Pro5    | Yes          | n.d.   | . 2  | SOHCYAGSGCPL1 FNVTSKTT |
| 32-1611     | mouse   | n.d.    | Yes          | n.d.   | yes  |                        |
| 304-1A5     | mouse   | n.d.    | Yes          | n.d.   | yes  |                        |
| 98-1F4      | mouse   | n.d.    | Yes          | n.d.   | . 01 |                        |
|             |         |         |              |        |      |                        |
|             |         |         | Fig 1        |        |      |                        |

Fig. 14

pc.h.mam.6a1.cell-57.579.1.t7

CACCATGGAGACAGGCCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCA GTCGCTGGAGGAGTCCGGCGGTCGCCTGGTAACGCCTGGAGGATCCCTGACACTCACCTGCAC AGTCTCTGGAATCGACCTCAGTAGCTATGGAGTGGGCTGGGTCCGCCAGGCTCCAGGGAAGG GGCTGGAATACATCGGAATCATTAGTAAAATTGATAACACATACTACGCGAACTGGGCGAAA GGCCGATTCACCATCTCCAAAACCTCGTCGACCACGGTGGATCTGAAAATGACCAGTCTGACA ACCGAGGACACGGCCACCTATTTCTGTACCAGAGGGTCTTTTGATCCCTGGGGCCCAGGCACC CTGGTCACCGTCTCCTCAGGGCAACCTAA A harmonia

pc.h.mam.16d8.cell-22.394.1.t7

CACCATGGAGACAGGCCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCA
GTCGGTGGAGGCTCCGGGGGTCGCCTGGTCACGCCTGGACACCCCTGCAC
AGTCTCTGGATTCTCCCTCAGCAGCTACGACATGACCTGGGTCCGCCAGGCTCCAGGGAAGGG
GCTGGAATGGATCGGAACCATTAGTACTATTGGTAGCCCATTTTACGCGAGCTGGGCGAGAGG
CCGATTCACCATCTCCAAAACCTCGACCACGGTGGATCTGAAAATCACCAATCCGACAACCGA
GGACACGGCCACGTATTTTTGCGGCAGATTTCGGATTGCTGGTGA TGGTGCCTTCTGGGGCCC
AGGCACGCTGGTCACCGTCTCCTCAGGGCAACCTAA

pc.h.mam.16d8.cell-21.393.2.t7

CACCATGGAGACAGGCCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCA
GTCGGTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTAGGACACCCCTGACACTCACCTGCAC
AGTCTCTGGATTCTCCCTCAGCAGCTACGACATGACCTGGGTCCGCCAGGCTCCAGGGAAGGG
GCTGGAATGGATCGGAACCATTAGTACTATTGGTAGCCCATTTTACGCGACCTGGGCGAGAGG
CCGATTCACCATCTCCAAAACCTCGACCACGGTGGATCTGAAAATCACCAATCCGACAACCGA
GGACACGGCCACGTATTTTTGCGGCAGATTTCGGATTGCTGGTGATGGTGCCTTCTGGGGCCC
AGGCACGCTGGTCACCGTCTCCTCAGGGCAACCTAA

pc.h.mam.6b12.cell-19.339.4.t7

CACCATGGAGACAGGCCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAAGGTGTCCGGTGTCA
GTCGGTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGAGATTCACCTGCAC
AGTCTCTGGAATCGACCTCAGCACCTACGACATGACCTGGGTCCGCCAGGCTCCAGGGAAGG
GACTGGAATGGATCGGAACCATTAGTACTCTTGGTACCCCTTTTTCCGCCAATTGGGCGAGAG
GCCGATTCACCATCTCCAAGACCTCGACCACGGTGGATCTGAAAATCGCCAGTCCGACGACCG
AAGACACTGCCACATATTTTTGTGGCAGATTGCGGATTGCTCATGATGGTGCCTTCTTGGGGCC
CAGGCACGCTGGTCACCGTCTCCTCAGGGCAACCTAA

pc.h.mam.2d3.cell-65.576.1.t7

CCCATGGAGACAGGCCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAG
GAGCAGCTGAAGGAGTCCGGAGGAGGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTG
CACAGTGTCTGGAATCGACCTCAATATCGATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGA
AGGGGCTGGAATGGATCGGAATTATTGGTACTCGTGGTGGCACATGGTTCGCGAGCTGGGCG
AAAGGCCGATTCACCATCTCCAAAACCCCGACCACAGTGGATCTGAAAATCCCCAGTCCGAC
AACCGAGGACACGGCCACCTATTTCTGTGCCAGTATCTATTCTGATAGTGGTACTTATACGAC
CTTGTGGGGCCCCAGGCACCCCGGTCACCGTCTCCTCAGGGCAACCTAA

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CACCATGGAGACAGGCCTGCGCTGGCTTCTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCA
GTCGGTGGAGGAGTCCGGGGGTCGCCTGGTCACCCTGGGACACCCCTGACACTCACCTGCAC
CGTCTCTGGATTCTCCCTCAGCAGCGTCGACATGACCTGGGTCCGCCAGGCTCCAGGGAAGGG
GCTGGAATGGATCGGAACCATTAGTACTCGTAGTAGCACATACTACGCGAGCTGGGCGAAAG
GCCGATTCACCATCTCCAAAACCTCGACCACGGTGGATCTGAAAATCACCAGTCCGACAACCG
AGGACACGGCCACGTATTTCTGTGGCAGATTTCGGATTGCTGGTGATGGTGCCTTCTGGGGCC
CAGGCACGCTGGTCACCGTCTCCTCAGGGCAACCTAA

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ATTTTCCCTCAGTAGCTGGTCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATG
GATCGGAATGATTGGTATTGTTGGTAGTGGCACATAATANGCGACCTGGGCGAAAGGCCGAT
TCACCATTTCCAAAACCTTGTGACCACGGTCGATTTGAAAATGACCAGTTTGACAACCGAGGA
CACGGCCACCTATTTTTGTGTCAGAGGGGGTAGTTTTANTTTTGCTACCGCCTTGTGGGGCCCA
GGCACCCTGGTCACCGTNTCCTCAGGGCAACCTAA

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TTGCAGGCTGCGTGGTTTTCCTGGTCGCTGTGCTCAAAGGTGTCCAGTGTCAGTCGGTGGAGG
AGTCCGGGGGTNGCCTGGTAACNCCTGGGACACCCCTGACANTTTTTTGCAAAGTNTTTGGAT
TTTCCCTCAGCAGNTACGANATGACCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATGG
ATNGGAACCATTAGTANTTGTGGTAATGGATAATACGCGACCTGGGCGAAAGGCCGATTCAC
CATTTCCAAAACCTTGACCACCGTGGATTTGAAAATCACCAGTCCGACAACCGAGGACACGG
CCAAGTATTTTTGTGGCAGATTTCGGATTGCTGGTGATGGTGCTTTTTGGGGCCCGGGCACGCT
GGTCACCGTNTCCTCAGGGCAACCTAA